REMARKS

The specification has been amended to correct references to certain SEQ ID NOs in the sequence listing. These sequences are correctly referenced elsewhere in the application, for example, at p. 3, lines 4-12, where the amino acid sequences of SEQ ID NO:1 and SEQ ID NO:2 are described, the polynucleotide sequences of SEQ ID NO:3 and SEQ ID NO:20, and their respective fragments and variants. The claims have been amended to clarify the invention. In particular, claim 1 has been amended to recite "the complement thereof" and "naturally occurring" variants. Claim 3 has also been amended to recite "the complement thereof", as well as antigenic and biologically active fragments of SEQ ID NO:2. Claim 4 has been amended at c) to delete reference to specific variant sequences of SEQ ID NOs:1 and 2, and to recite "a naturally occurring variant of SEQ ID NO:3 or SEQ ID NO:20 having at least 90% sequence identity to SEQ ID NO:3 or SEQ ID NO:20". Support for the phrase "naturally occurring" as recited in claims 1 and 4 is found in the specification, for example, at p. 12, line 41, and at p. 13, line 2 which recite "naturally occurring genes' and polynucleotides encoding "naturally occurring ARP". The "complement" of a cDNA is specifically defined in the specification at p. 6, lines 30-32. Support for the amendments to claim 3 reciting an "antigenic epitope" or "biologically active portion" of SEQ ID NO:20 is found in the specification, for example, at p. 11, lines 9-12. Support for the amendment to claim 4 reciting variant polynucleotide sequences, is found in the specification, for example, at p. 9, lines 9-15, and in the Table at p. 12 of that specification where variant polynucleotide sequences of SEQ ID NOs:3 and 20 having from about 80% to about 100% sequence identity to SEQ ID NOs: 3 and 20 are described. No new matter is added by these amendments, and entry of the amendments is therefore requested.

Restriction Requirement

The Examiner acknowledged Applicants election without traverse (underline added) filed July 2, 2002 and that it has been entered. The Examiner stated, however, that in reply to the Office Action mailed June 4, 2002, Applicants elected Group II, claims 1 and 3-8 but failed to elect a single disclosed species of the invention as required.

In response to the Restriction Requirement, Applicants point out that the response filed July 2, 2002 elected the claims of Group II with traverse (see p. 3, line 7) and the species of polynucleotide encoding SEQ ID NO:2, i.e., SEQ ID NO:20, again with traverse (p. 3, lines9-10). Reasons for the traverse were given in the balance of the response at pp. 3 and 4. Applicants therefore submit that the election, with traverse, was properly made and supported. Applicants further surmise that the failure to elect a single

disclosed species as the present Restriction Requirement recites relates to the Examiner's statement at the first paragraph of p. 8 of the previous Restriction Requirement that claim 4 is further generic to a plurality of patentably distinct species comprising fragments of SEQ ID NO:20 selected from SEQ ID NOs:21-39, and required Applicant to also elect a single disclosed species from this Group. In response to this requirement, Applicants choose the species of SEQ ID NO:21, again with traverse for the reasons previously cited in the response filed July 2, 2002. See, in particular, p. 3, second paragraph of that response.

Applicants therefore reiterate their request for reconsideration of the Restriction Requirement and examination of claims 1-14 in Groups I-VI with respect to all species recited. In the event that the Examiner maintains the Restriction Requirement, the Examiner is reminded that claims 9-14 of Groups IV and VI are methods of use of the compositions of Group II that depend from and are of the same scope as the claims of Group II , and are subject to rejoinder on allowance of the claims of Group II in accordance with *Ochiai and Brouwer* regardless of their restriction (see Commissioner's Notice in the Official Gazette of March 26, 1996). Applicants reserve the right to prosecute the subject matter of non-elected claims in subsequent divisional applications.

Applicants believe that no fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Deposit Account No. 09-0108.

Respectfully submitted,

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Date: August 22, 2002

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Version with markings t show changes made

IN THE SPECIFICATION

Paragraph beginning at line 20 of page 9 has been amended as follows:

Nucleic acids encoding the ARP-1 of the present invention were first identified in Incyte Clone 1555118 from the human bladder tumor cDNA library (BLADTUT04) using a computer search for amino acid sequence alignments. A consensus sequence, **SEQ ID NO:[2]3**, was derived from the following overlapping and/or extended nucleic acid sequences (SEQ ID NO:4-11): Incyte Clones 1555118H1 (BLADTUT04), 7227391H1 (BRAXTDR15), 70158486V1 (SG0000039), 70162686V1 (SG0000040), 70151326V1 (SG0000038), 70154198V1 (SG0000038), 2084238T6 (UTRSNOT08), 70155923V1 (SG0000038), and GenBank EST g6661750 (SEQ ID NO:57), and edited Genscan sequence GNN.g10801482_004.edit (SEQ ID NO:58). For sequence GNN.g10801482_004.edit, coding regions were predicted by Genscan analysis of the genomic DNA. g10801482 is the GenBank identification number of the sequence to which Genscan was applied.

Paragraph beginning at line 12 of page 10 has been amended as follows:

Nucleic acids encoding the ARP-2 of the present invention were first identified in Incyte Clone 2582063 from the human bladder tumor cDNA library (KIDNTUT13) using a computer search for amino acid sequence alignments. A consensus sequence, **SEQ ID NO:20**, was derived from the following overlapping and/or extended nucleic acid sequences (**SEQ ID NO:21-39[4-11]**): Incyte Clones 2582063H1 (KIDNTUT13), 7246093H1 (PROSTMY01), 7978420H1, 55040412H1, 2929484F6 (TLYMNOT04), 5627320R8 (PLACFER01), 3209128F6 (BLADNOT08), 349248H1 (LVENNOT01), 7019961H1 (PANCNON03), 6303175H2 (TLYMUNT02), 2549906F6 (LUNGTUT06), 1945452H1 (PITUNOT01), 2549906T6 (LUNGTUT06), 71009002V1 (SG0000308), 71008521V1 (SG0000308), 71010168V1 (SG0000308), 70090181V1 (SG0000030), 6833928H1 (BRSTNON02), 70089663V1 (SG0000030), and GenBank ESTs g6993427 (SEQ ID NO:59), g5529915 (SEQ ID NO:60), and g1733437 (SEQ ID NO:61).

IN THE CLAIMS:

Claims 1 and 3- 4 has been amended as follows:

1. (Twice Amended) An isolated cDNA, or the complement thereof, encoding a protein having the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2, or a naturally occurring variant of SEQ ID NO:1 or SEQ ID NO:2 having at least 95% amino acid identity to SEQ ID NO:1 or SEQ ID NO:2.

3. (Once Amended) An isolated cDNA, or the complement thereof, encoding a protein having the amino acid sequence of SEQ ID NO:2, an antigenic epitope of SEQ ID NO:2, or a biologically active portion of SEQ ID NO:2.

4. (Once Amended) An isolated cDNA selected from:

a) a nucleic acid sequence of SEQ ID NO:3 or SEQ ID NO:20 or the complement thereof;

b) a fragment of SEQ ID NO:3 selected from SEQ ID NOs:4-11 or the complement thereof or a fragment of SEQ ID NO:20 selected from SEQ ID NOs:21-39 or the complement thereof; and

c) a naturally occurring variant of SEQ ID NO:3 [selected from SEQ ID NOs:12-19] or [a variant of] SEQ ID NO:20 having at least 90% sequence identity to SEQ ID NO:3 or SEQ ID NO:20 [selected from SEQ ID NOs:40-56].